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1 GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTGTCTCTGCTCGCCCGCTG 60
-----+-----+-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGGCGGAC
 M H S L G F F S V A C S L L A A A -
61 CGCTGCTCCCGGCTCCTCGGAGGGCGCGCGCGCGCGCGCTTTCGAGTCCGGACTCG 120
-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGCGCCAGGAGCGCTCCGCGGGCGGGCGGGCGGGAAGCTCAGGCCCTGAGC
 L L P G P R E A P A A A A A F E S G L D -
121 ACCTCTCGGACGGGAGCCCGACGGGGCGGAGGCCACGGCTTATGCAAGCAAGATCTGG 180
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCTCGGGCTCGGCCCGCTCCGGTGCCGAATACGTTCTGTTCTAGACC
 L S D A E P D A G E A T A Y A S K D L E -
181 AGGAGCAGTTACGGTCTGTGTCCAGTGATGAAGTCACTGACTGTACTCTACCCAGAAT 240
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
 E Q L R S V S S V D E L M T V L Y P E Y -
241 ATTGGAAAATGTACAAGTGCAGCTAAGGAAGGAGGCTGGCAACATAACAGAGAACAGG 300
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCTTCTCCGACCGTTGTATTGTCTCTGTCTCC
 W K M Y K C Q L R K G G W Q H N R E Q A -
 CCAACTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG

Fig. 1A

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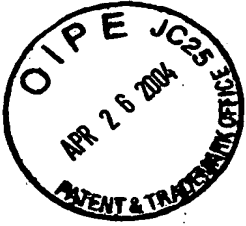
[illegible]

Fig. 1B



661 TTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720
-----+-----+-----+-----+-----+-----+
AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG
Y R Q V H S I I R R S L P A T L P Q C Q -
721 AGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAAATAATCACATCTGCAGATGCC 780
-----+-----+-----+-----+-----+-----+
TCCGTCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTACCGG
A A N K T C P T N Y M W N N H I C R C L -
781 TGGCTCAGGAAGATTTTATGTTTCCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840
-----+-----+-----+-----+-----+-----+
ACCGAGTCCTTCTAAATAACAAAGAGCCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D S T D G F H -
841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCTCAGTGTGTCTGCAGAG 900
-----+-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTGTTCCTCGACCTACTTCTCTGGACAGTCAACACAGACGTCTC
D I C G P N K E L D E E T C Q C V C R A -
901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT 960
-----+-----+-----+-----+-----+-----+
GCCCCGAGCCGGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C -
961 GTGTCTGTAAAAACAACCTCTTCCCCAGCCCAATGTGGGGCCCAACCGAGAAATTGTATGAAA 1020
-----+-----+-----+-----+-----+-----+
CACAGACATTTTGTGAGAAAGGGTCGGTTACACCCCGGTGGCTCTTAAACTACTTT

Fig.1C



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V C K N K L F P S Q C G A N R E F D E N -
ACACATGCCAGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080
-----+-----+-----+-----+-----+
TGTTACGGTCACACATACATTTCTTGGACGGGCTCTTAGTGGGATTTAGGACCTT
T C C Q C V C K R T C P R N Q P L N P G K -
AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC 1140
-----+-----+-----+-----+-----+
TTACACGGACACTTACATGTCTTTCAGGTGCTCTTACGAACAATTTCTCTTCAAGG
C A C E C T E S P Q K C L L K G K K F H -
ACCACCAACATGCAGCTGTACAGACGGCCCATGTACGAACCCGACAGAGGCTTGTGAGC 1200
-----+-----+-----+-----+-----+
TGGTGGTTTGTPACGTCGACAAATGTCTGCCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
H Q T C S C Y R R P C T N R Q K A C E P -
CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCAATATTGGCAAAGACCAC 1260
-----+-----+-----+-----+-----+
GTCCATAAAGTATATCACTTCTTACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
G F S Y S E E V C R C V P S Y W Q R P Q -
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT

Fig. 1D

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[illegible]

Fig. 1E